

Open reading frame 1a, Alignment of aminoacid sequence of PRRS virus strain ATCC VR-2332

1 MSGILDRCTC TPNARVFM AE GQVYCTRCLS ARSLLPLNLQ VSELGVLGLF YRPEEPLRWT  
61 LPRAFFTVEC SPAGACWLSA IFPIARMTSG NLNFQQRMRV VAAELYRAGQ LTPAVLKALQ  
121 VYERGCWYP IVGPVPGVAV FANSLHVSDK PFPGATHVLT NLPLQRPKP EDFCFECAM  
181 ATVYDIGHDA VMYVAERKVS WAPRGDEVK FEAVPGELKL IANRLRTSFP PHHTVDMSE  
241 AFTAPGCGVS MRVERQHGCL PADTVPEGNC WWSLFDLLPL EVQNKIRHA NQFGYQTKHG  
301 VSGYLQRRLL QVNGLRVTD LNGPIVVQYF SVKESWIRHL KLAGEPSYSG FEDLLRIRVE  
361 PNTSPLADKE EKIFRFGSHK WYGAGKRARK ARSCATATVA GRALSVRETR QAKEHEVAGA  
421 NKAHLKHYS PPAEGNCGWH CISAIANRMV NSKFETLPE RVRPPDDWAT DEDLVNAIQI  
481 LRLPAALDRN GACTSAKYVL KLEGEHWTVT VTPGMSPSLL PLECVQGCCG HKGGLGSPDA  
541 VEVSGFDPAC LDRLAEVMHL PSSAIPAALA EMSGSDSRSA SPVTTVWTVS QFFARHSGGN  
601 HPDQVRLGKI ISLCQVIEDC CCSQNKTNRV TPEEVAAKID IYLRGATNLE ECLARLEKAR

Fig. 1

661 PPRVIDTSFD WDVVLPQVEA ATQTIKLPQV NQCRALVPV TQKSLDNNV PLTAFSLANY  
721 YYRAQGEVR HRERLTAVLS KLEKVVREY GLMTEPGPR PTLPRGLDEL KDQMEEDLLK  
781 LANAQTSDM MAWAVEQVDL KTWVKNYPRW TTPPPPPKVQ PRKTKPVKSL PERKVPVAPR  
841 RKGSDCGSP VSLGGDVPNS WEDLAVSSPF DLTPPEPAT PSSELVIVSS PQCIFRPATP  
901 LSEPAPIPAP RGTVSRPVTP LSEPIVPAP RRKFQQVKRL SSAAAIPPYQ DEPLDLSASS  
961 QTEYEASPPA PPQGGVLGV EGHEAEETLS EISDMSGNIK PASVSSSSSL SSVRITRPKY  
1021 SAQAIIIDSGG PCSGHLQEVK ETCLSVMREA CDATKLDDBA TQEWLSRMWD RVDMLTWRNT  
1081 SVYQAICTLD GRKFLPKMI LETPPYPCE FVMHPHPAP SVGAESDLTI GSVATEDVPR  
1141 ILEKIENVGE MANQPLAFS EDKPVDDQLV NDPRISSRP DESTSAPSAG TGGAGSFTDL  
1201 PPSDGADADG GGPFRTVKRK AERLFDQLSR QVEDLVSHLP VFFSRLFYPG GGYSPPGDWGF  
1261 AAFLLCLFL CYSYPAFGIA PLLGVFSGSS RVRMGVFGC WLAFVGLFK PVSDPVGAAC

1321 EFDSPECRNI LHSFELLKPW DPVRSLVVGP VGLGLAILGR LLGGARCIWH FLRLGIVAD  
1381 CILAGAYVLS QGRCKKCWGS CIRTAPNEVA FNVFFTRAT RSSLIDLCDR FCAPKGMDFI  
1441 FLATGWRGCW AGRSPIEQPS EKPIAFAQLD EKKITARTVV AQPYDPNQAV KCLRVLQSGG  
1501 RWWSLG-PKS GQFRCIPS PFFPTGVKVD PDCRVVDDPD TFTAALRSY STTNVLVGVG  
1561 DFAQLNGLKI RQISKPSGGG PHLMAALHVA CSMALHMLAG IYVTAVGSCG TGTNDPWCAN  
1621 PFAVPGYGP SLCTSRLCIS QHGLTLPLTA LVAGFGIQEI ALVVLIFVSI GGMAHRLSCK  
1681 ADMLCVLLAI ASYVWVPLTW LLCVFPCWLR CFSLHPLTIL WLVEFLISVN MPGILAMVL  
1741 LVSLWLLGRY TNVAGLVTPY DIHHYTSQPR GVAALATAPD GTYLAARRA ALTGRTMLFT  
1801 PSQLGSLLEG AFRTRKPSLN TVNVIGSSMG SGGVFTIDGK VKCVTAAHVL TGNSARVSGV  
1861 GFNQMLDFDV KGDFAIADCP NWQGAAPKTQ FCTDGTGTRA YWLTSSGVEP GVIGKGFAFC  
1921 FTACGDSGSP VITEAGELVG VHTGSNKQGG GIVTRPSQGF CNVAPIKLSE LSEFFAGPKV  
1981 PLGDVKVGSH IIKDISEVPS DLCALLAAKP ELEGGLSTVQ LLCVFFLLWR MMGHAWTPLV

Fig. 1b

2041 AVSFFILNEV LPAVLVRSVF SFGMFVLSWL TPWSAQVIMI RLLTAALNRN RWSLAFFSLG  
2101 AVTGEVADLA ATQGHPLQAV MNLSTYAFLP RMMVVTSPVP VITCGVVHLL AIILYLFKYR  
2161 GPHHILVGDG VFSAAFFLRY FAEGKLREGV SOSCGMNHES LTGALAMRLN DEDLDFLMKW  
2221 TDFKCFVSAS NMRNAAGQFI EAAYAKALRV ELAQLVQVDK VRGTLAKLEA FADTVAPQLS  
2281 PGDIVVALGH TPVGSIFDLK VGSTKHTLQA IETRVLAGSK MTVARVVDPT PTPPPAPVPI  
2341 PLPPKVLENG PNAWGDEDL NKKKRRRMEA LGIYVMGKK YQKFDKNSG DVFYEEVHNN  
2401 TDEWECLRVG DPADFPEKG TLCGHVTIEN KAYHVTSPS GKKFLVPVNP ENGRVQWEAA  
2461 KLSVEQALGM MNVDGELTAK ELEKLRIID KLQGLTKEQC LNC\*

Fig. 1c

Open reading frame 1b, Alignment of aminoacid sequence of PRRS virus strain ATCC VR-2332

1 LAASDLTRCG RGGLVVTETA VKIVKFHNRT FTLGPVNLKV ASEVELKDAV EHNQHPVARP  
61 IDGGVLLRS AVPSLIDVLI SGADASPKLL AHGPGNTGI DGTLDWFESE ATKEEVALSA  
121 QIIQACDIRR GDAPEIGLPY KLYPVRGNPE RVKGVLQNTR FGDIPYKTPS DTGSPVHAAA  
181 CLTPNATPVT DGRSVLATM PPGFELYVPT IPASVLDYLD SRPDCPKQLT EHGCEDAALK  
241 DLSKYDLSTQ GFVLPGLRL VRKYLFAHVG KCPPVHRPST YPAKNMAGI NGNRFP TKDI  
301 QSVPEIDVLC AQAVRENWQT VTPCTLKKQY CGKKKTRTIL GTNNFIALAH RAVLSGVTQG  
361 FMKKAFNSPI ALGKNKFKEL QTPVLGRCL EADLASC DRST PAIVRWFAAN LIYELACAE E  
421 HLP SYVLNCC HDLLVTQSGA VTKRGLLSSG DPITSVSNTI YSLVIYAQHM VLSYFKSGHP  
481 HGLLFLQDQL KFE DMLKVQP LIVYSDDDLVL YAESPTMPNY HWWVEHLNLM LGFQTDPKKT  
541 AITDSPSFLG CRIINGRQLV PNRDRILAAL AYHMKASNV EYASAAAAIL MDSCACLEYD  
601 PEWFEELVVG IAQCARKDGY SFPGTFFMS MWEKLSN YE GKKS RVC GYC GAPAPYATAC

Fig. 2

661 GLDVCYHHTH FHQHCPTIWIW CGHPAGSGSC SECKSPVGKG TSPIDEVLEQ VPKPPRTVI  
721 MHVEQGLTPL DPGRYQTRRG LVSRRRGIRG NEUGLPDGDY ASTALLPTCK EINMVAVASN  
781 VLRSRFLIGP PGAGKTYWLL QQVQDGDVIY TPTHQTMLDM IRALGTCRFN VPAGTTLQFP  
841 VPSRTGPWVR ILAGGWCPCGK NSFLDEAAYC NHLDVLRLLS KTTLTCLGDF KQLHPVGFDS  
901 HCVVFDIMPO TQLKTIWRFQ QNICDAIQPD YRDKLMSMVN TTRVTYVEKP VRYGQVLTPIY  
961 HRDREDDAIT IDSSQGATFD VVTLHLPTKD SLNRQALVA ITRARHAIFV YDPHRQLQGL  
1021 FDLPAKGTPV NIAVHCDGQL IVLDRNNKEC TVAQALNGD KFRATDKRVV DSLRAICADL  
1081 EGSSSPLPKV AHNLGIFYFSP DLTQFAKLPV ELAPHWPVVS TONNEKWPDR LVASLRPIHK  
1141 YSRACIGAGY MVGPSVFLGT PGVVSYYLTK FVKGGAQVLP ETVFSTGRIE VDCREYLDNR  
1201 EREVAASLPH GFIGDVKGTT VGGCHHVTSR YLPRVLPKES VAVVGVSPPG KAAKALCTLT  
1261 DVYLPDLEAY LHPETQSKCW KMMLDFKEVR LMVWKDKTAY FQLEGRYFTW YQLASYASYI

Fig. 2a

1321 RVPVNSTVYL DPCMGPALCN RRVVGSTHWG ADLAVTPYDY GAKIILSSAY HGEMPPGYKI

1381 LACAEFSLDD PVKYKHTWGF ESDTAYLYEF TGNGEDWEDY NDAFRARQEG KIYKATATSL

1441 KFYFFPGPVI EPTLGLN\*

Fig. 2b

Open reading frame 2, Alignment of aminoacid sequence of PRRS virus strain ATCC VR-2332

1 MKWGPCKAFL TKLANFLWML SRSSWCPLLI SLYFWPFCLA SPSVVGWWSF ASDWEAPRYS  
61 VRALPFTLSN YRRSYEAFLS QCQVDIPTWG TKHPLGLMLWH HKVSTLIDEM VSRRMYRIME  
121 KAGQAANKQV VSEATLSRIS SLDVVAHFQH LAAIEAETCK YLASRLPMLH NLRMTGSNVT  
181 IVYNSTLNQV FAIFPTPGSR PKLHDFQQWL IAVHSSIFSS VAASCTLFVV LWLRVPILRT  
241 VFGFRWLGA I FLSNSQ\*

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Fig. 3



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VR 2332	10 ATGTCTGGGA	20 TACTTGATCG	30 GTGCACGTGT	40 ACCCCCAATG	50 CCAGGGTGTT	60 TATGGCGGAG
VR 2332	70 GGCCAAGTCT	80 ACTGCACACG	90 ATGCCTCAGT	100 GCACGGTCTC	110 TCCTTCCCCT	120 GAACCTCCAA
VR 2332	130 GTTTCTGAGC	140 TCGGGGTGCT	150 AGGCCTATTC	160 TACAGGCCCG	170 AAGAGCCACT	180 CCGGTGGACG
VR 2332	190 TTGCCACGTG	200 CATTCCCCAC	210 TGTTGAGTGC	220 TCCCCGCCG	230 GGGCCTGCTG	240 GCTTTCTGCA
VR 2332	250 ATCTTTCCAA	260 TCGCACGAAT	270 GACCAGTGGA	280 AACCTGAACT	290 TCCAACAAAG	300 AATGGTACGG
VR 2332	310 GTCGCAGCTG	320 AGCTTTACAG	330 AGCCGGCCAG	340 CTCACCCCTG	350 CAGTCTTGAA	360 GGCTCTACAA
VR 2332	370 GTTTATGAAC	380 GGGGTTGCCG	390 CTGGTACCCC	400 ATTGTTGGAC	410 CTGTCCCTGG	420 AGTGGCCGTT
VR 2332	430 TTCGCCAATT	440 CCCTACATGT	450 GAGTGATAAA	460 CCTTTCCCGG	470 GAGCAACTCA	480 CGTGTTGACC
VR 2332	490 AACCTGCCGC	500 TCCCGCAGAG	510 ACCCAAGCCT	520 GAAGACTTTT	530 GCCCCTTTGA	540 GTGTGCTATG
VR 2332	550 GCTACTGTCT	560 ATGACATTGG	570 TCATGACGCC	580 GTCATGTATG	590 TGGCCGAAAG	600 GAAAGTCTCC
VR 2332	610 TGGGCCCTC	620 GTGGCGGGGA	630 TGAAGTGAAA	640 TTTGAAGCTG	650 TCCCCGGGGA	660 GTTGAAGTTG
VR 2332	670 ATTGCGAACC	680 GGCTCCGCAC	690 CTCCTTCCCG	700 CCCCACCACA	710 CAGTGGACAT	720 GTCTAAGTTC
VR 2332	730 GCCTTCACAG	740 CCCCTGGGTG	750 TGGTGTTTCT	760 ATGCGGGTCG	770 AACGCCAACA	780 CGGCTGCCTT
VR 2332	790 CCCCTGACA	800 CTGTCCCTGA	810 AGGCAACTGC	820 TGGTGGAGCT	830 TGTTTGACTT	840 GCTTCCACTG
VR 2332	850 GAAGTTCAGA	860 ACAAAGAAAT	870 TCGCCATGCT	880 AACCAATTG	890 GCTACCAGAC	900 CAAGCATGGT
VR 2332	910 GTCTCTGGCA	920 AGTACCTACA	930 GCGGAGGCTG	940 CAAGTTAATG	950 GTCTCCGAGC	960 AGTAACTGAC
VR 2332	970 CTAAACGGAC	980 CTATCGTCGT	990 ACAGTACTTC	1000 <u>TCCGTTAAGG</u>	1010 AGAGTTGGAT	1020 CCGCCATTG
VR 2332	1030 AAACTGGCGG	1040 GAGAACCCAG	1050 CTACTCTGGG	1060 TTTGAGGACC	1070 TCCTCAGAAT	1080 AAGGGTTGAG
VR 2332	1090 CCTAACACGT	1100 CGCCATTGGC	1110 TGACAAGGAA	1120 GAAAAAATTT	1130 TCCGGTTTGG	1140 CAGTCACAAG
VR 2332	1150 TGGTACGGCG	1160 CTGGAAAGAG	1170 AGCAAGAAAA	1180 GCACGCTCTT	1190 GTGCGACTGC	1200 TACAGTCGCT
VR 2332	1210 GGCCGCGCTT	1220 TGTCCGTTCG	1230 TGAAACCCGG	1240 CAGGCCAAGG	1250 AGCACGAGGT	1260 TGCCGGCGCC

Fig. 4

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VR 2332	1270 AACAAAGGCTG	1280 AGCACCTCAA	1290 ACACTACTCC	1300 CCGCCTGCCG	1310 AAGGGAATTG	1320 TGGTTGGCAC
VR 2332	1330 TGCATTTCCG	1340 CCATCGCCAA	1350 CCGGATGGTG	1360 AATTCCAAAT	1370 TTGAAACCAC	1380 CCTTCCCGAA
VR 2332	1390 AGAGTGAGAC	1400 CTCCAGATGA	1410 CTGGGCTACT	1420 GACGAGGATC	1430 TTGTGAATGC	1440 CATCCAAATC
VR 2332	1450 CTCAGACTCC	1460 CTGCGGCCTT	1470 AGACAGGAAC	1480 GGTGCTTGTA	1490 CTAGCGCCAA	1500 GTACGTACTT
VR 2332	1510 AAGCTGGAAG	1520 GTGAGCATTG	1530 GACTGTCACT	1540 GTGACCCCTG	1550 GGATGTCCCC	1560 TTCTTTGCTC
VR 2332	1570 CCTCTTGAAT	1580 GTGTTTCAGGG	1590 CTGTTGTGGG	1600 CACAAGGGCG	1610 GTCTTGGTTC	1620 CCCAGATGCA
VR 2332	1630 GTCGAGGTCT	1640 CCGGATTTGA	1650 CCCTGCCTGC	1660 CTTGACCGGC	1670 TGGCTGAGGT	1680 GATGCACCTG
VR 2332	1690 CCTAGCAGTG	1700 CTATCCCAGC	1710 CGCTCTGGCC	1720 GAAATGTCTG	1730 GCGATTCCGA	1740 TCGTTCCGGCT
VR 2332	1750 TCTCCGGTCA	1760 CCACCGTGTG	1770 GACTGTTTCG	1780 CAGTTCCTTG	1790 CCCGTCACAG	1800 CGGAGGGAAT
VR 2332	1810 CACCTGACC	1820 AAGTGCGCTT	1830 AGGGAAAATT	1840 ATCAGCCTTT	1850 GTCAGGTGAT	1860 TGAGGACTGC
VR 2332	1870 TGCTGTTCCC	1880 AGAACAAAAC	1890 CAACCGGGTC	1900 ACCCCGGAGG	1910 AGGTCGCAGC	1920 AAAGATTGAC
VR 2332	1930 CTGTACCTCC	1940 GTGGTGCAAC	1950 AAATCTTGAA	1960 GAATGCTTGG	1970 CCAGGCTTGA	1980 GAAAGCGCGC
VR 2332	1990 CCGCCACGCG	2000 TAATCGACAC	2010 CTCCTTTGAT	2020 TGGGATGTTG	2030 TGCTCCCTGG	2040 GGTTGAGGCG
VR 2332	2050 GCAACCCAGA	2060 CGATCAAGCT	2070 GCCCCAGGTC	2080 AACCAGTGTC	2090 GTGCTCTGGT	2100 CCCTGTTGTG
VR 2332	2110 ACTCAAAAGT	2120 CCTTGACAA	2130 CAACTCGGTC	2140 CCCCTGACCG	2150 CCTTTTCACT	2160 GGCTAACTAC
VR 2332	2170 TACTACCGTG	2180 CGCAAGGTGA	2190 CGAAGTTCGT	2200 CACCGTGAAA	2210 GACTAACCGC	2220 CGTGCTCTCC
VR 2332	2230 AAGTTGGAAA	2240 AGGTTGTTCG	2250 AGAAGAATAT	2260 GGGCTCATGC	2270 CAACCGAGCC	2280 TGGTCCACGG
VR 2332	2290 CCCACACTGC	2300 CACGCGGGCT	2310 CGACGAACTC	2320 AAAGACCAGA	2330 TGGAGGAGGA	2340 CTTGCTGAAA
VR 2332	2350 CTGGCTAACG	2360 CCCAGACGAC	2370 TTCGGACATG	2380 ATGGCCTGGG	2390 CAGTCGAGCA	2400 GGTTGACCTA
VR 2332	2410 AAAACCTGGG	2420 TCAAGAACTA	2430 CCCGCGGTGG	2440 ACACCACCAC	2450 CCCCTCCGCC	2460 AAAAGTTTCA
VR 2332	2470 CCTCGAAAAA	2480 CGAAGCCTGT	2490 CAAGAGCTTG	2500 CCGGAGAGAA	2510 AGCCTGTCCC	2520 CGCCCCGCGC

Fig. 4a

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VR 2332	2530 AGGAAGGTTG	2540 GGTCCGATTG	2550 TGGCAGCCCG	2560 GTTTCATTAG	2570 GCGGCGATGT	2580 CCCTAACAGT
VR 2332	2590 TGGGAAGATT	2600 TGGCTGTTAG	2610 TAGCCCCTTT	2620 GATCTCCCGA	2630 CCCCACCTGA	2640 GCCGGCAACA
VR 2332	2650 CCTTCAAGTG	2660 AGCTGGTGAT	2670 TGTGTCCTCA	2680 CCGCAATGCA	2690 TCTTCAGGCC	2700 GGCGACACCC
VR 2332	2710 TTGAGTGAGC	2720 CGGCTCCAAT	2730 TCCCGCACCT	2740 CGCGGAACTG	2750 TGTCTCGACC	2760 GGTGACACCC
VR 2332	2770 TTGAGTGAGC	2780 CGATCCCTGT	2790 GCCCCGACCG	2800 CGGCGTAAGT	2810 TTCAGCAGGT	2820 GAAAAGATTG
VR 2332	2830 AGTTCGGCGG	2840 CGGCAATCCC	2850 ACCGTACCAG	2860 GACGAGCCCC	2870 TGGATTTGTC	2880 TGCTTCCTCA
VR 2332	2890 CAGACTGAAT	2900 ATGAGGCCTC	2910 TCCCCAGCA	2920 CCGCCGCAGA	2930 GCGGGGGCGT	2940 TCTGGGAGTA
VR 2332	2950 GAGGGGCATG	2960 AAGCTGAGGA	2970 AACCCTGAGT	2980 GAAATCTCGG	2990 ACATGTCGGG	3000 TAACATTAAA
VR 2332	3010 CCTGCGTCCG	3020 TGTCATCAAG	3030 CAGCTCCTTG	3040 TCCAGCGTGA	3050 GAATCACACG	3060 CCCAAATAC
VR 2332	3070 TCAGCTCAAG	3080 CCATCATCGA	3090 CTCGGGCGGG	3100 CCCTGCAGTG	3110 GGCATCTCCA	3120 AGAGGTAAAG
VR 2332	3130 GAAACATGCC	3140 TtagTGTcat	3150 GCGCGAGGCA	3160 TGTGATGCGA	3170 CTAAGCTTGA	3180 TGACCCTGCT
VR 2332	3190 ACGCAGGAAT	3200 GGCTTTCTCG	3210 CATGTGGGAT	3220 CGGGTGGACA	3230 TGCTGACTTG	3240 GCGCAACACG
VR 2332	3250 TCTGTTTACC	3260 AGGCGATTTG	3270 CACCTTAGAT	3280 GGCAGGTTAA	3290 AGTTCCTCCC	3300 AAAAATGATA
VR 2332	3310 CTCGAGACAC	3320 CGCCGCCCTA	3330 TCCGTGTGAG	3340 TTTGTGATGA	3350 TGCCTCACAC	3360 GCCTGCACCT
VR 2332	3370 TCCGTAGGTG	3380 CGGAGAGCGA	3390 CCTTACCATT	3400 GGCTCAGTTG	3410 CTACTGAAGA	3420 TGTTCCACGC
VR 2332	3430 ATCCTCGAGA	3440 AAATAGAAAA	3450 TGTCGGCGAG	3460 ATGGCCAACC	3470 AGGGACCCTT	3480 GGCCTTCTCC
VR 2332	3490 GAGGATAAAC	3500 CGGTAGATGA	3510 CCAACCTGTC	3520 AACGACCCCC	3530 GGATATCGTC	3540 GCGGAGGCCT
VR 2332	3550 GACGAGAGCA	3560 CATCAGCTCC	3570 GTCCGCAGGC	3580 ACAGGTGGCG	3590 CCGGCTCTTT	3600 TACCGATTTG
VR 2332	3610 CCGCCTTCAG	3620 ATGGCGCGGA	3630 TGCGGACGGG	3640 GGGGGGCCGT	3650 TTCGGACGGT	3660 AAAAAGAAAA
VR 2332	3670 GCTGAAAGGC	3680 TCTTTGACCA	3690 ACTGAGCCGT	3700 CAGGTTTTTG	3710 ACCTCGTCTC	3720 CCATCTCCCT
VR 2332	3730 GTTTTCTTCT	3740 CACGCCTTTT	3750 CTACCCTGGC	3760 GGTGGTTATT	3770 CTCCGGGTGA	3780 TTGGGGTTTT

Fig. 4b

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VR 2332	3790 GCAGCTTTTA	3800 CTCTATTGTG	3810 CCTCTTTTTA	3820 TGTTACAGTT	3830 ACCCAGCCTT	3840 TGGTATTGCT
VR 2332	3850 CCCCCTCTTG	3860 GTGTGTTTTT	3870 TGGGTCTTCT	3880 CGGCGCGTTC	3890 GAATGGGGGT	3900 TTTTGGCTGC
VR 2332	3910 TGGTTGGCTT	3920 TTGCTGTTGG	3930 TCTGTTCAAG	3940 CCTGTGTCCG	3950 ACCCAGTCGG	3960 CGCTGCTTGT
VR 2332	3970 GAGTTTGACT	3980 CGCCAGAGTG	3990 TAGAAACATC	4000 CTTCATTCTT	4010 TTGAGCTTCT	4020 CAAACCTTGG
VR 2332	4030 GACCCTGTTC	4040 GCAGCCTTGT	4050 TGTGGGCCCC	4060 GTCGGTCTCG	4070 GTCTTGCCAT	4080 TCTTGGCAGG
VR 2332	4090 TTACTGGGCG	4100 GGGCACGCTG	4110 CATCTGGCAC	4120 TTTTTGCTTA	4130 GGCTTGGCAT	4140 TGTTGCAGAC
VR 2332	4150 TGTATCTTGG	4160 CTGGAGCTTA	4170 CGTGCTTTCT	4180 CAAGGTAGGT	4190 GTAAAAAGTG	4200 CTGGGGATCT
VR 2332	4210 TGTATAAGAA	4220 CTGCTCCTAA	4230 TGAGGTCGCT	4240 TTTAACGTGT	4250 TTCCTTTCAC	4260 ACGTGCGACC
VR 2332	4270 AGGTCGTCAC	4280 TTATCGACCT	4290 GTGCGATCGG	4300 TTTTGTGCGC	4310 CAAAAGGAAT	4320 GGACCCCAT
VR 2332	4330 TTTCTCGCCA	4340 CTGGGTGGCG	4350 CGGGTGCTGG	4360 GCCGGCCGAA	4370 GCCCCATTGA	4380 GCAACCCTCT
VR 2332	4390 GAAAAACCCA	4400 TCGCGTTTGC	4410 CCAATTGGAT	4420 GAAAAGAAGA	4430 TTACGGCTAG	4440 GACTGTGGTC
VR 2332	4450 GCCCAGCCTT	4460 ATGACCCCAA	4470 CCAAGCCGTA	4480 AAGTGCTTGC	4490 GGGTATTGCA	4500 GTCGGGTGGG
VR 2332	4510 CGATGGTGGC	4520 TAAGCGGTCC	4530 CAAAAGTGGT	4540 CAAGGTTTCC	4550 GCTGTTCCAT	4560 TCCGAGCCCC
VR 2332	4570 TTCTTTCCCA	4580 CTGGAGTGAA	4590 AGTTGACCCT	4600 GATTGCAGGG	4610 TCGTGGTTGA	4620 CCCTGACACT
VR 2332	4630 TTCACGTCAG	4640 CTCTCCGGTC	4650 TGGCTACTCC	4660 ACCACAAACC	4670 TCGTCCTTGG	4680 TGTAGGGGAC
VR 2332	4690 TTTGCCCAGC	4700 TGAATGGATT	4710 AAAAATCAGG	4720 CAAATTTCCA	4760 AGCCTTCAGG	4740 GGGAGGCCCA
VR 2332	4750 CATCTCATGG	4760 CTGCCCTGCA	4770 TGTTGCCTGC	4780 TCGATGGCTC	4790 TGCACATGCT	4800 TGCTGGGATT
VR 2332	4810 TATGTGACTG	4820 CGGTGGGTTC	4830 TTGCGGCACC	4840 GGCACCAACG	4850 ACCCGTGGTG	4860 CGCTAACCCG
VR 2332	4870 TTTGCCGTCC	4880 CTGGCTACGG	4890 ACCTGGCTCT	4900 CTCTGCACGT	4910 CCAGGTTGTG	4920 CATTTCCCAA
VR 2332	4930 CACGGCCTTA	4940 CCCTGCCCTT	4950 GACAGCACTT	4960 GTGGCGGGAT	4970 TCGGTATTCA	4980 AGAAATTGCC
VR 2332	4990 TTGGTCGTTT	5000 TGATTTTTGT	5010 TTCCATCGGA	5020 GGCATGGCTC	5030 ATAGGTTGAG	5040 CTGTAAGGCT

Fig. 4c

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VR 2332	5050 GACATGCTGT	5060 GTGTTTTGCT	5070 TGCAATTGCC	5080 AGCTATGTTT	5090 GGGTACCTCT	5100 TACCTGGTTG
VR 2332	5110 CTTTGTGTGT	5120 TTCCTTGCTG	5130 GTTGCGCTGT	5140 TTTCTTTTGC	5150 ACCCCTCAC	5160 CATCCTATGG
VR 2332	5170 TTGGTGTTTT	5180 TCCTTGATTC	5190 TGTGAATATG	5200 CCTTCAGGAA	5210 TCCTGGCCAT	5220 GGTGTTGTTG
VR 2332	5230 GTTTCTCTTT	5240 GGCTTCTTGG	5250 TCGTTATACT	5260 AATGTTGCTG	5270 GCCTTGTCAC	5280 CCCCTACGAC
VR 2332	5290 ATTCATCATT	5300 ACACCAGTGG	5310 CCCCCGCGGT	5320 GTTGCCGCCT	5330 TGGCTACCGC	5340 ACCAGATGGG
VR 2332	5350 ACCTACTTGG	5360 CCGCTGTCCG	5370 CCGCGCTGCG	5380 TTGACTGGCC	5390 GCACCATGCT	5400 GTTTACCCCG
VR 2332	5410 TCCCAGCTTG	5420 GGTCTCTTCT	5430 TGAGGGTGCT	5440 TTCAGAACTC	5450 GAAAGCCCTC	5460 ACTGAACACC
VR 2332	5470 GTCAATGTGA	5480 TCGGGTCTCT	5490 CATGGGCTCT	5500 GGCGGGGTGT	5510 TTACCATCGA	5520 CGGGAAAGTC
VR 2332	5530 AAGTGCGTAA	5540 CTGCCGCACA	5550 TGTCTTACG	5560 GGCAATTCAG	5570 CTCGGGTTTC	5580 CGGGGTCCGC
VR 2332	5590 TTCAATCAAA	5600 TGCTTGACTT	5610 TGACGTAAAG	5620 GGAGATTTTCG	5630 CTATAGCTGA	5640 TTGCCCGAAT
VR 2332	5650 TGGCAAGGGG	5660 CTGCCCCCAA	5670 GACCCAATTC	5680 TGCACGGATG	5690 GATGGACTGG	5700 CCGTGCCTAT
VR 2332	5710 TGGCTAACAT	5720 CCTCTGGCGT	5730 CGAACCCGGC	5740 GTCATTGGAA	5750 AAGGATTCGC	5760 CTTCTGCTTC
VR 2332	5770 ACCGCATGTG	5780 GCGATTCCGG	5790 GTCCCCAGTG	5800 ATCACCGAGG	5810 CCGGTGAGCT	5820 TGTCGGCGTT
VR 2332	5830 CACACGGGAT	5840 CGAATAAACA	5850 AGGGGGGGGC	5860 ATTGTTACGC	5870 GCCCCTCAGG	5880 CCAGTTTTGT
VR 2332	5890 AATGTGGCAC	5900 CCATCAAGCT	5910 AAGCGAATTA	5920 AGTGAATTCT	5930 TTGCTGGGCC	5940 TAAGGTCCCC
VR 2332	5950 CTCGGTGATG	5960 TGAAGGTCGG	5970 CAGCCACATA	5980 ATTAAAGACA	5990 TAAGCGAGGT	6000 GCCTTCAGAT
VR 2332	6010 CTTTGTGCCT	6020 TGCTTGCTGC	6030 CAAACCTGAA	6040 CTGGAAGGAG	6050 GCCTCTCCAC	6060 CGTCCAACTT
VR 2332	6070 CTTTGTGTGT	6080 TTTTTCTCCT	6090 GTGGAGAATG	6100 ATGGGACATG	6110 CCTGGACGCC	6120 CTTGGTTGCT
VR 2332	6130 GTGAGTTTCT	6140 TTATTTTGAA	6150 TGAGGTTCTC	6160 CCAGCCGTCC	6170 TGGTCCGGAG	6180 TGTTTTCTCC
VR 2332	6190 TTTGGAATGT	6200 TTGTGCTATC	6210 CTGGCTCACG	6220 CCATGGTCTG	6230 CGCAAGTTCT	6240 GATGATCAGG
VR 2332	6250 CTTCTGACAG	6260 CAGCTCTTAA	6270 CAGGAACAGA	6280 TGGTCACTTG	6290 CCTTTTTTCAG	6300 CCTCGGTGCA

Fig. 4d

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VR 2332	6310 GTGACCGGTT	6320 TTGTGCGAGA	6330 TCTTGCGGGC	6340 ACTCAGGGGC	6350 ATCCGTTGCA	6360 GGCAGTGATG
VR 2332	6370 AATTTGAGCA	6380 CCTATGCATT	6390 CCTGCCTCGG	6400 ATGATGGTTG	6410 TGACCTCACC	6420 AGTCCCAGTG
VR 2332	6430 ATCACGTGTG	6440 GTGTGCGTGA	6450 CCTACTTGCC	6460 ATCATTTTGT	6470 ACTTGTTTAA	6480 GTACCGTGCC
VR 2332	6490 CCGCACCATA	6500 TCCTTGTTGG	6510 CGATGGAGTG	6520 TTCTCTGCGG	6530 CTTCTCTCTT	6540 GAGATACTTT
VR 2332	6550 GCCGAGGGAA	6560 AGTTGAGGGA	6570 AGGGGTGTG	6580 CAATCCTGCG	6590 GAATGAATCA	6600 TGAGTCTCTG
VR 2332	6610 ACTGGTGCCC	6620 TCGCTATGAG	6630 ACTCAATGAC	6640 GAGGACTTGG	6650 ATTTCTTTAT	6660 GAAATGGACT
VR 2332	6670 GATTTTAAGT	6680 GCTTTGTTTC	6690 TGCCTCCAAC	6700 ATGAGGAATG	6710 CAGCGGGTCA	6720 ATTTATCGAG
VR 2332	6730 GCTGCCTATG	6740 CTAAAGCACT	6750 TAGAGTAGAA	6760 CTGGCCCAGT	6770 TGGTGCCAGT	6780 TGATAAAGTT
VR 2332	6790 CGAGGTACTT	6800 TGGCCAAACT	6810 TGAAGCTTTT	6820 GCTGATACCG	6830 TGGCACCTCA	6840 ACTCTCGCCC
VR 2332	6850 GGTGACATTG	6860 TTGTGCTCT	6870 CGGCCACACG	6880 CCTGTTGGCA	6890 GTATCTTCGA	6900 CCTAAAGGTT
VR 2332	6910 GGTAGCACCA	6920 AGCATACCCT	6930 CCAAGCCATT	6940 GAGACCAGAG	6950 TCCTTGCTGG	6960 GTCCAAAATG
VR 2332	6970 ACCGTGGCGC	6980 GCGTCGTCGA	6990 CCCGACCCCC	7000 ACGCCCCCAC	7010 CCGCACCCGT	7020 GCCCATCCCC
VR 2332	7030 CTCCCACCGA	7040 AAGTTCTGGA	7050 GAATGGCCCC	7060 AACGCTTGCG	7070 GGGATGAGGA	7080 CCGTTTGAAT
VR 2332	7090 AAGAAGAAGA	7100 GGCGCAGGAT	7110 GGAAGCCCTC	7120 GGCATCTATG	7130 TTATGGGCGG	7140 GAAAAAGTAC
VR 2332	7150 CAGAAATTTT	7160 GGGACAAGAA	7170 TTCCGGTGAT	7180 GTGTTTTATG	7190 AGGAGGTCCA	7200 TAATAACACA
VR 2332	7210 GATGAGTGGG	7220 AGTGTCTCAG	7230 AGTTGGCGAC	7240 CCTGCCGACT	7250 TTGACCCTGA	7260 GAAGGGAAGT
VR 2332	7270 CTGTGTGGAC	7280 ATGTCACCAT	7290 TGAAAACAAG	7300 GCTTACCATG	7310 TTTACACCTC	7320 CCCATCTGGT
VR 2332	7330 AAGAAGTTCT	7340 TGGTCCCCGT	7350 CAACCCAGAG	7360 AATGGAAGAG	7370 TTCAATGGGA	7380 AGCTGCAAAG
VR 2332	7390 CTTTCCGTGG	7400 AGCAGGCCCT	7410 AGGTATGATG	7420 AATGTCGACG	7430 GCGAACTGAC	7440 TGCCAAAGAA
VR 2332	7450 CTGGAGAAAC	7460 TGAAAAGAAT	7470 AATTGACAAA	7480 CTCCAGGGCC	7490 TGACTAAGGA	7500 GCAGTGTTTA
VR 2332	7509 AACTGCTAG					

Fig. 4e

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VR 2332	10	20	30	40	50	60
	CTAGCCGCCA	GCGACTTGAC	CCGCTGTGGT	CGCGGCGGCT	TGGTTGTTAC	TGAAACAGCG
VR 2332	70	80	90	100	110	120
	GTAAAAATAG	TCAAATTTCA	CAACCGGACC	TTCACCCTGG	GACCTGTGAA	TTTAAAAAGTG
VR 2332	130	140	150	160	170	180
	GCCAGTGAGG	TTGAGCTAAA	AGACGCGGTT	GAGCACAACC	AACACCCGGT	TGCGAGACCG
VR 2332	190	200	210	220	230	240
	ATCGATGGTG	GAGTTGTGCT	CCTGCGTTCC	GCGGTTCCCT	CGCTTATAGA	CGTCTTGATC
VR 2332	250	260	270	280	290	300
	TCCGGTGCTG	ATGCATCTCC	CAAGTTACTT	GCCCATCACG	GGCCGGGAAA	CACTGGGATC
VR 2332	310	320	330	340	350	360
	GATGGCACGC	TCTGGGATTT	TGAGTCCGAA	GCCACTAAAG	AGGAAGTCGC	ACTCAGTGCG
VR 2332	370	380	390	400	410	420
	CAAATAATAC	AGGCTTGTGA	CATTAGGCGC	GGCGACGCTC	CTGAAATTGG	TCTCCCTTAC
VR 2332	430	440	450	460	470	480
	AAGCTGTACC	CTGTTAGGGG	TAACCCTGAG	CGGGTGAAAG	GAGTTCCTGA	GAATACAAGG
VR 2332	490	500	510	520	530	540
	TTTGGAGACA	TACCTTACAA	AACCCCAGT	GACACTGGAA	GCCCAGTGCA	CGCGGCTGCC
VR 2332	550	560	570	580	590	600
	TGCCTTACGC	CCAACGCCAC	TCCGGTGACT	GATGGGCGCT	CCGTCTTGGC	CACGACCATG
VR 2332	610	620	630	640	650	660
	CCCCCGGGT	TTGAGTTATA	TGTACCGACC	ATACCAGCGT	CTGTCCTTGA	TTACCTTGAC
VR 2332	670	680	690	700	710	720
	TCTAGGCCTG	ACTGCCCTAA	ACAGCTGACA	GAGCACGGCT	GCGAAGATGC	CGCACTGAAA
VR 2332	730	740	750	760	770	780
	GACCTCTCTA	AATATGACTT	GTCCACCCAA	GGCTTTGTTT	TACCTGGAGT	TCTTCGCCTT
VR 2332	790	800	810	820	830	840
	GTGCGGAAAT	ACCTGTTTGC	CCATGTAGGT	AAGTGCCAC	CCGTTTCATCG	GCCTTCTACT
VR 2332	850	860	870	880	890	900
	TACCCTGCTA	AGAATTCTAT	GGCTGGAATA	AATGGGAACA	GGTTCCCAAC	CAAGGACATT
VR 2332	910	920	930	940	950	960
	CAGAGCGTCC	CTGAAATCGA	CGTTCTGTGC	GCACAGGCTG	TGCGAGAAAA	CTGGCAAAC
VR 2332	970	980	990	1000	1010	1020
	GTCACCCCTT	GTA CTCTTAA	GAAACAGTAT	TGCGGGAAGA	AGAAGACTAG	GACCATACTC
VR 2332	1030	1040	1050	1060	1070	1080
	GGCACCAATA	ACTTCATCGC	ACTAGCCCAC	CGAGCAGTGT	TGAGTGGTGT	TACCCAGGGC
VR 2332	1090	1100	1110	1120	1130	1140
	TTTATGAAAA	AGGCGTTTAA	CTCGCCCATC	GCCCTCGGAA	AGAACAAGTT	TAAGGAGCTA
VR 2332	1150	1160	1170	1180	1190	1200
	CAGACTCCGG	TCCTGGGCAG	GTGCCTTGAA	GCTGATCTCG	CATCCTGCGA	TCGATCCACG
VR 2332	1210	1220	1230	1240	1250	1260
	CCTGCAATTG	TCCGCTGGTT	TGCCGCCAAC	CTTCTTTATG	AACTTGCCTG	TGCTGAAGAG

Fig. 5

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VR 2332	1270 CATCTACCGT	1280 CGTACGTGCT	1290 GAACTGCTGC	1300 CACGACTTAC	1310 TGGTCACGCA	1320 GTCCGGCGCA
VR 2332	1330 GTGACTAAGA	1340 GAGGTGGCCT	1350 GTCGTCTGGC	1360 GACCCGATCA	1370 CCTCTGTGTC	1380 TAACACCATT
VR 2332	1390 TATAGTTTGG	1400 TGATCTATGC	1410 ACAGCATATG	1420 GTGCTTAGTT	1430 ACTTCAAAAG	1440 TGGTCACCCC
VR 2332	1450 CATGGCCTTC	1460 TGTTCTTACA	1470 AGACCAGCTA	1480 AAGTTTGAGG	1490 ACATGCTCAA	1500 GGTTCAACCC
VR 2332	1510 CTGATCGTCT	1520 ATTTCGGACGA	1530 CCTCGTGCTG	1540 TATGCCGAGT	1550 CTCCCACCAT	1560 GCCAAACTAT
VR 2332	1570 CACTGGTGGG	1580 TTGAACATCT	1590 GAATTTGATG	1600 CTGGGGTTTC	1610 AGACGGACCC	1620 AAAGAAGACA
VR 2332	1630 GCAATAACAG	1640 ACTCGCCATC	1650 ATTTCTAGGC	1660 TGTAGAATAA	1670 TAAATGGGCG	1680 CCAGCTAGTC
VR 2332	1690 CCCAACCGTG	1700 ACAGGATCCT	1710 CGCGGCCCTC	1720 GCCTATCACA	1730 TGAAGGCGAG	1740 TAATGTTTCT
VR 2332	1750 GAATACTATG	1760 CCTCAGCGGC	1770 TGCAATACTC	1780 ATGGACAGCT	1790 GTGCTTGTTT	1800 GGAGTATGAT
VR 2332	1810 CCTGAATGGT	1820 TTGAAGAACT	1830 TGTAAGTTGA	1840 ATAGCGCAGT	1850 GCGCCCGCAA	1860 GGACGGCTAC
VR 2332	1870 AGCTTTCCCG	1880 GCACGCCGTT	1890 CTTCATGTCC	1900 ATGTGGGAAA	1910 AACTCAGGTC	1920 CAATTATGAG
VR 2332	1930 GGGAAGAAGT	1940 CGAGAGTGTG	1950 CGGGTACTGC	1960 GGGGCCCCGG	1970 CCCCGTACGC	1980 TACTGCCTGT
VR 2332	1990 GGCCTCGACG	2000 TCTGCATTTA	2010 CCACACCCAC	2020 TTCCACCAGC	2030 ATTGTCCAGT	2040 CACAATCTGG
VR 2332	2050 TGTGGCCATC	2060 CAGCGGGTTC	2070 TGTTTCTTGT	2080 AGTGAGTGCA	2090 AATCCCCTGT	2100 AGGGAAAGGC
VR 2332	2110 ACAAGCCCTT	2120 TAGACGAGGT	2130 GCTGGAACAA	2140 GTCCCGTATA	2150 AGCCCCCAGC	2160 GACCGTTATC
VR 2332	2170 ATGCATGTGG	2180 AGCAGGGTCT	2190 CACCCCCCTT	2200 GATCCAGGTA	2210 GATACCAAAC	2220 TCGCCGCGGA
VR 2332	2230 TTAGTCTCTG	2240 TCAGGCGTGG	2250 AATTAGGGGA	2260 AATGAAGTTG	2270 GACTACCAGA	2280 CGGTGATTAT
VR 2332	2290 GCTAGACCGG	2300 CCTTGCTCCC	2310 TACCTGCAAA	2320 GAGATCAACA	2330 TGGTCGCTGT	2340 CGCTTCCAAT
VR 2332	2350 GTATTGCGCA	2360 GCAGGTTTCAT	2370 CATCGGCCCA	2380 CCCGGTGCTG	2390 GGAAAACATA	2400 CTGGCTCCTT
VR 2332	2410 CAACAGGTCC	2420 AGGATGGTGA	2430 TGTTATTTAC	2440 ACACCAACTC	2450 ACCAGACCAT	2460 GCTTGACATG
VR 2332	2470 ATTAGGGCTT	2480 TGGGGACGTG	2490 CCGGTTCAAC	2500 GTCCCGGCAG	2510 GCACAACGCT	2520 GCAATTCCCC

Fig. 5a



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VR 2332	2530 GTCCCCCTCCC	2540 GCACCGGTCC	2550 GTGGGTTCGC	2560 ATCCTAGCCG	2570 GCGGTTGGTG	2580 TCCTGGCAAG
VR 2332	2590 AATTCCTTCC	2600 TAGATGAAGC	2610 AGCGTATTGC	2620 AATCACCTTG	2630 ATGTTTTGAG	2640 GCTTCTTAGT
VR 2332	2650 AAAACCTACCC	2660 TCACCTGTCT	2670 AGGAGACTTC	2680 AAGCAACTCC	2690 ACCCAGTGGG	2700 TTTTGATTCT
VR 2332	2710 CATTGCTATG	2720 TTTTTGACAT	2730 CATGCCTCAA	2740 ACTCAACTGA	2750 AGACCATCTG	2760 GAGGTTTGGA
VR 2332	2770 CAGAATATCT	2780 GTGATGCCAT	2790 TCAGCCAGAT	2800 TACAGGGACA	2810 AACTCATGTC	2820 CATGGTCAAC
VR 2332	2830 ACAACCCGTG	2840 TGACCTACGT	2850 GGAAAAACCT	2860 GTCAGGTATG	2870 GGCAGGTCCT	2880 CACCCCCTAC
VR 2332	2890 CACAGGGACC	2900 GAGAGGACGA	2910 CGCCATCACT	2920 ATTGACTCCA	2930 GTCAAGGCGC	2940 CACATTCGAT
VR 2332	2950 GTGGTTACAT	2960 TGCATTTGCC	2970 CACTAAAGAT	2980 TCACTCAACA	2990 GGCAAAGAGC	3000 CCTTGTTGCT
VR 2332	3010 ATCACCAGGG	3020 CAAGACACGC	3030 TATCTTTGTG	3040 TATGACCCAC	3050 ACAGGCAGCT	3060 GCAGGGCTTG
VR 2332	3070 TTTGATCTTC	3080 CTGCAAAAGG	3090 CACGCCCGTC	3100 AACCTCGCAG	3110 TGCCTGCGA	3120 CGGGCAGCTG
VR 2332	3130 ATCGTGCTGG	3140 ATAGAAATAA	3150 CAAAGAATGC	3160 ACGTTTGCTC	3170 AGGCTCTAGG	3180 CAACGGGGAT
VR 2332	3190 AAATTTAGGG	3200 CCACAGACAA	3210 GCGTGTTGTA	3220 GATTCTCTCC	3230 GCGCCATTTG	3240 TGCTGATCTA
VR 2332	3250 GAAGGGTCGA	3260 GCTCTCCGCT	3270 CCCCAAGGTC	3280 GCACACAAC	3290 TGGGATTTTA	3300 TTTCTCACCT
VR 2332	3310 GATTTAACAC	3320 AGTTTGCTAA	3330 ACTCCCAGTA	3340 GAACTTGCAC	3350 CTCACTGGCC	3360 CGTGGTGTCA
VR 2332	3370 ACCCAGAACA	3380 ATGAAAAGTG	3390 GCCGGATCGG	3400 CTGGTTGCCA	3410 GCCTTCGCCC	3420 TATCCATAAA
VR 2332	3430 TACAGCCGCG	3440 CGTGCAATCGG	3450 TGCCGGCTAT	3460 ATGGTGGGCC	3470 CTTCGGTGTT	3480 TCTAGGCACT
VR 2332	3490 CCTGGGGTCG	3500 TGTCATACTA	3510 TCTCACAAAA	3520 TTTGTTAAGG	3530 GCGGGGCTCA	3540 AGTGCTTCCG
VR 2332	3550 GAGACGGTTT	3560 TCAGCACCGG	3570 CCGAATTGAG	3580 GTAGACTGCC	3590 GGGAATATCT	3600 TGATGATCGG
VR 2332	3610 GAGCGAGAAG	3620 TTGCTGCGTC	3630 CCTCCCACAC	3640 GGTTTCATTG	3650 GCGACGTCAA	3660 AGGCACTACC
VR 2332	3670 GTTGGAGGAT	3680 GTCATCATGT	3690 CACCTCCAGA	3700 TACCTCCCGC	3710 GCGTCCTTCC	3720 CAAGGAATCA
VR 2332	3730 GTTGCGGTAG	3740 TCGGGGTTTC	3750 AAGCCCCGGA	3760 AAAGCCGCGA	3770 AAGCATTGTG	3780 CACACTGACA

Fig. 5b

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VR 2332	3790 GATGTGTACC	3800 TCCCAGATCT	3810 TGAAGCCTAT	3820 CTCCACCCGG	3830 AGACCCAGTC	3840 CAAGTGCTGG
VR 2332	3850 AAAATGATGT	3860 TGGACTTCAA	3870 AGAAGTTCGA	3880 CTAATGGTCT	3890 GGAAAGACAA	3900 AACAGCCTAT
VR 2332	3910 TTCCAACCTG	3920 AAGGTCGCTA	3930 TTTCACCTGG	3940 TATCAGCTTG	3950 CCAGCTATGC	3960 CTCGTACATC
VR 2332	3970 CGTGTTCCCG	3980 TCAACTCTAC	3990 GGTGTAATTG	4000 GACCCCTGCA	4010 TGGGCCCCGC	4020 CCTTTGCAAC
VR 2332	4030 AGGAGAGTCG	4040 TCGGGTCCAC	4050 CCACTGGGGG	4060 GCTGACCTCG	4070 CGGTCACCCC	4080 TTATGATTAC
VR 2332	4090 GGCGCTAAAA	4100 TTATCCTGTC	4110 TAGCGCGTAC	4120 CATGGTGAAA	4130 TGCCCCCCGG	4140 ATACAAAATT
VR 2332	4150 CTGGCGTGCG	4160 CGGAGTTCTC	4170 GTTGGATGAC	4180 CCAGTTAAGT	4190 ACAAACATAC	4200 CTGGGGGTTT
VR 2332	4210 GAATCGGATA	4220 CAGCGTATCT	4230 GTATGAGTTC	4240 ACCGGAAACG	4250 GTGAGGACTG	4260 GGAGGATTAC
VR 2332	4270 AATGATGCGT	4280 TTCGTGCGCG	4290 CCAGGAAGGG	4300 AAAATTTATA	4310 AGGCCACTGC	4320 CACCAGCTTG
VR 2332	4330 AAGTTTTATT	4340 TTCCCCCGGG	4350 CCCTGTCATT	4360 GAACCAACTT	4374 TAGGCCTGAA	TTGA

Fig. 5c

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VR 2332	10 ATGAAATGGG	20 GTCCATGCAA	30 AGCCTTTT <u>TTG</u>	40 ACAAAATTGG	50 CCAACTTTTT	60 GTGGATGCTT
VR 2332	70 TCACGGAGTT	80 CTTGGTGTCC	90 ATTGTTGATA	100 TCATTATATT	110 TTTGGCCATT	120 TTGTTTGGCT
VR 2332	130 TCACCATCGC	140 CGGTTGGCTG	150 GTGGTCTTTT	160 GCATCAGATT	170 GGTTTGCTCC	180 GCGATACTCC
VR 2332	190 GTACGCGCCC	200 TGCCATTAC	210 TCTGAGCAAT	220 TACAGAAGAT	230 CTTATGAGGC	240 CTTTCTTTCC
VR 2332	250 CAGTGCCAAG	260 TGGACATTCC	270 CACCTGGGGA	280 ACTAAACATC	290 CTTTGGGGAT	300 GCTTTGGCAC
VR 2332	310 CATAAGGTGT	320 CAACCCTGAT	330 TGATGAAATG	340 GTGTCGCGTC	350 GAATGTACCG	360 CATCATGGAA
VR 2332	370 AAAGCAGGGC	380 AGGCTGCCTG	390 GAAACAGGTG	400 GTGAGCGAGG	410 CTACGCTGTC	420 TCGCATTAGT
VR 2332	430 AGTTTGGATG	440 TGGTGGCTCA	450 TTTTCAGCAT	460 CTAGCCGCCA	470 TTGAAGCCGA	480 GACCTGTAAA
VR 2332	490 TATTTGGCCT	500 CCCGGCTGCC	510 CATGCTACAC	520 AACCTGCGCA	530 TGACAGGGTC	540 AAATGTAACC
VR 2332	550 ATAGTGTATA	560 ATAGCACTTT	570 GAATCAGGTG	580 TTTGCTATTT	590 TTCCAACCCC	600 TGGTTCCCGG
VR 2332	610 CCAAAGCTTC	620 ATGATTTTCA	630 GCAATGGTTA	640 ATAGCTGTAC	650 ATTCCCTCCAT	660 ATTTTCCTCT
VR 2332	670 GTTGCAGCTT	680 CTTGTA CTCT	690 TTTGTGTGTG	700 CTGTGGTTGC	710 GGGTTC CAAT	720 ACTACGTACT
VR 2332	730 GTTTTTGGTT	740 TCCGCTGGTT	750 AGGGGCAATT	760 TTTCTTTTCA	770 ACTCACAGTG	A

Fig. 6